

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 16, 2000, 15:37:36 ; Search time 151.92 Seconds
(without alignments)
5342.438 Million cell updates/sec

Title: US-09-211-755-1
Perfect score: 3244
Sequence: 1 TGACCTCGGGCAGGTCCTG.....CTTGCAAAAAAAAAAAAA 3244

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N_Geneseq_36.*

Word size : 0

Number of hits that pass the threshold : 623170

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	317.2	9.8	2924	1	V10267	Human GABA-BR1b re
2	315.2	9.7	2620	1	V10265	Human GABA-BR1a/b
3	312.8	9.6	2837	1	V10266	Rat GABA-BR1b rece
4	306	9.4	4376	1	V10264	Rat GABA-BR1a rece
5	286.8	8.8	314	1	V88919	EST clone HW456. N
6	177	5.5	361	1	X51891	Human secreted pro
7	45.4	1.4	2176	1	Q11726	Sequence encoding
8	45.4	1.4	397	1	X51965	Human secreted pro
9	43.6	1.3	15872	1	Q10613	Rianodin receptor
10	42.4	1.3	273	1	V89458	EST clone CO337. N
11	42.4	1.3	114955	1	X53491	Human adenosine A1
12	41.8	1.3	1312	1	Q73383	Human CCAAT/Enhanc
13	41.8	1.3	1312	1	T44325	DNA encoding CCAAT
14	41.6	1.3	8438	1	Q73500	DNA encoding Pseud
15	41.6	1.3	2823	1	T35233	Natural killer lyt
16	41.6	1.3	2888	1	T53268	Streptomyces prist
17	41	1.3	2618	1	T16710	Metabotropic gluta
18	41	1.3	2619	1	T29408	Human metabotropic
19	41	1.3	4131	1	T89290	Dogfish shark kidn
20	40.6	1.3	3865	1	Q37101	Bovine transglutam
21	40.6	1.3	10596	1	Q51731	Plasmod pcisEBON f
22	40.6	1.3	10596	1	T40348	Vector plasmod pCM
23	40.6	1.3	9600	1	V21683	Nucleotide sequenc
24	40.6	1.3	10596	1	X15650	Melanocortin-3 rec
25	40.4	1.2	1080	1	T68789	Human melanocortin
26	40.4	1.2	1080	1	Q06399	Melanocortin-3 rec
27	40.4	1.2	1080	1	V62351	Human MC3 DNA. Pro
28	40.4	1.2	1080	1	Q01963	Sequence of genom
29	40.4	1.2	1648	1	Q25532	Maize optimised ge
30	40.2	1.2	1158	1	V06396	Nucleotide sequenc
31	40.2	1.2	799	1	V55831	MH mutant porcine
32	39.8	1.2	15377	1	Q25975	Phospholipase D-p
33	39.4	1.2	2006	1	Q50147	Parathyroid calciu
34	39.2	1.2	5006	1	T61381	Parathyroid calciu
35	39.2	1.2	3809	1	T61382	Nuclear mitotic ap
36	39.2	1.2	1041	1	T77781	E6AP-binding prote
37	39.2	1.2	1092	1	T78310	Nucleotide sequenc
38	39.2	1.2	4000	1	T86166	Human parathyroid
39	39.2	1.2	5006	1	T95858	

40	39.2	1.2	3809	1	T95859	Human parathyroid
41	39.2	1.2	5006	1	V26963	Human parathyroid
42	39.2	1.2	3809	1	V26964	Human parathyroid
43	39.2	1.2	5006	1	V82484	Human parathyroid
44	39.2	1.2	3809	1	V82485	Human parathyroid
45	39	1.2	1312	1	T93367	Mouse thrombin rec

ALIGNMENTS

RESULT 1
V10267
ID V10267 standard; cDNA to mRNA; 2924 BP.
AC V10267;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1b receptor cDNA.
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 169..2703
FT /*tag= a
FT /product= GABA-BR1b
PN WO9746675-A1.
PD 11-DEC-1997.
PF 19-MAR-1997; E01370.
PR 22-NOV-1996; US-756091.
PS 30-MAY-1996; US-655716.
PA (NOVS) NOVARTIS AG.
PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
DR WPI: 98-042183/04.
DR P-FSDB; W40119.
PT Purified GABA-B receptor or receptor protein - and antagonists of
these which may be useful in treating nervous system disorders
PS Claim 3; Page 79-86; 108pp; English.
CC This cDNA sequence encodes a novel human GABA-B receptor protein,
GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory
neurotransmitter found in the brain and peripheral nervous system
and this receptor may be used for the identification of GABA-B
receptor agonists and antagonists. Such proteins may be used in
treatment of dementia, depression, anxiety, epilepsy, spasticity,
bronchial inflammation or asthma or to improve cognitive function.
CC GABA-B receptor ligands and probes derived from this sequence can be
used to assay for GABA-B receptors or DNA encoding them.
SQ Sequence 2924 BP; 628 A; 852 C; 793 G; 651 T;

Query Match 9.8%; Score 317.2; DB 1; Length 2924;
Best Local Similarity 48.2%; Pred. No. 3.3e-68;
Matches 1034; Conservative 0; Mismatches 1083; Indels 27; Gaps 4;

Qy	232	CCCCCGCGGCATGCCAGTGTGCCCGCGGCTCTGTCTAGCGCGCGCTCTCCATCATG	291
Db	271	CTCCCGCGGCTCACTCGGGTCTCCCGCCGCCCTCCAGAACGCGGCGAGTGTAC	330
Qy	292	GGCTCATGCGCTCACCAGGAGGTGGCCAGGCGAGCATCGGGCGGGTGTGTCTCCC	351
Db	331	ATCGGGGCACTGTTTCCCATGAGCGGGGGTGGCCAGGGGCCAGGCGCTGCCAGCGCG	390
Qy	352	GGCTGGAACCTGGCCATCGAGCAGATCCGGAACGAGTCACTCTCTGCGCCCTACTTCTC	411
Db	391	GTGAGATGGCGCTGGAGGACGTGAATAGCGGAGGACATCTCTCCGGACTATGAGCTC	450
Qy	412	GACCTGCGGCTCTATGACAGGATGGCAACAGCGCAAAAGGTTGAAAGCTTCTACGAT	471
Db	451	AAGCTCATCCACGACAGCAAGTGTGATCCAGGCCAACCCACCAAGTACCTATATGAG	510
Qy	472	CGGATAAATACGGCGCGACCACTTGTATGGTGTGTTGGAGCGGTCTGTCTCCGTCACA	531
Db	511	CTGCTTACAAACGACCTATCAA---GATCATCTTATGCTGCTGCTGCTGTCTCTCC	567

QY 532 TCCATCATGCGAGTCCCTCCAGGCTGGAATCTGGTGCAGCTTCTTTTGGTGCACCC 591
 Db 568 ACGCTGGTGGCTGAGGCTGCTAGGATGTGGAACTCATCTGCTTCTTCTATGGCTCCAGC 627
 QY 592 ACGCTGTTCTAGCGGATAAGAAAATACCCCTTATTTCTTTTGGACCGTCCCATACAGC 651
 Db 628 TCACAGCCCTGTCAACCGGCGAGCTTTCCCACTTTTCTTCCGAAGCCACCCATCAGCC 687
 QY 652 AATGGGTTGAATCCAGCAATCTCAAGCTTGTCTCAAGCACTACCAAGTGAAGCGGTGGGC 711
 Db 688 ACATCCCAACCCCTACCCGCTGAAACTCTTTGAAAAGTGGGCTGGAAGAAGATTGCT 747
 QY 712 ACGCTGAGCGAAGAGCTTCAGAGGTTCTCTGAGGTGGGAATGACCTGACTGAGATTCTG 771
 Db 748 ACCATCCAGCAGACCACTGAGGCTTCTACTTCGACTCTGGACGACCTGGAGAACAGTG 807
 QY 772 TATGGCGAGGACATGAGATTTAGACACCGAGAGCTTCTCCACAGATCCCTGTACCAGT 831
 Db 808 AAGGAGGCTGGAATTTGAGATTACTTTCCGCCAGAGTTTCTTCCAGATCCAGCTGTGCC 867
 QY 832 GTCAAAAGCTGAAGGGCAATGATGTGGGATCATCTTGGCCAGTTTGACCAAGATG 891
 Db 868 GTCAAAAGCTGAAGGGCAAGATGATGTGGGATCATCTTGGCCAGTTTGACCAAGATG 927
 QY 892 GCAGCAAAAGTGTCTGTTGTGCATACGAGGAGAACATGTATGTAGTAGTAATATCAGTGG 951
 Db 928 GCCCGAAAGTTTGTGAGGTGTACAAGGAGGCTCTCTTTGGGAAGAAGTACGTCTGG 987
 QY 952 ATCATTCGGGCTGTAGAGCTTCTTGGTGGAGAGTGTGCACAGGAAGCAATCA 1011
 Db 988 TTCTTCATGGGTGTATGTCTGACAAATTTGGT-----TCAAGATCTACGACCTTCT 1038
 QY 1012 TCCCGCTGCTCCGGAAGATCTGCTGCTGCATGGAGGCTACATTTGGCTGATTTTC 1071
 Db 1039 ATCAACTGCACAGTGGATGAGTACTGAGGGGTGGAGGCCACATCACAACCTGAGATT 1098
 QY 1072 GAGCCCTGAGCTTCCAGCAGATCAAGACCATCTCTAGGAAGATGCCACAGATATGAG 1131
 Db 1099 GTCATGCTGAATCTTGCCTCAATACCGCAGCATTTCCAACATGACATCCAGGAATTTGT 1158
 QY 1132 AGAGAGTCAACAAGCGGTGAG-----CGTGGGGCCAGCAAGTTCCAGGGGTAC 1185
 Db 1159 GAGAACTAACCAAGGCTGAAAAGACACCCCTGAGGAGAGAGAGGCTTCCAGGAGCA 1218
 QY 1186 GCCTACGATGGCATCTGGTCTATCCCAAGACATCTGCAGAGGGCCATGGAGACACTGCAT 1245
 Db 1219 CGCTGGCTATGATGCCATCTGGGCTTGGCACTGGCCCTGAACAAGACATCTGGAGGA 1278
 QY 1246 GCGAGAGCCGCGACCGAGGATCCAGGACTTCAACTACAGGAGCCACAAGCTGGGCGAGG 1305
 Db 1279 GCGGCGGCTTCTGTGTGGCGCTGGAGGACTTCAACTACAACAACAGCACCATACCGAC 1338
 QY 1306 ATCATCTCAATGCCATGACAGACCAACTCTTTCGGGTGACGGGTCAAGTTGATTTC 1365
 Db 1339 CAATCTACCGGGCAATGAATCTTCTGCTTGGAGGTGCTCTGGCCATGTGGTGTTT 1398
 QY 1366 CGGATGGGGAGAGATGGGGACCAATTAATTTACTTAATTTCAAGACAGCAGGGAGGTG 1425
 Db 1399 GATGCCAGCGCTCTCGGATGCGATGGAGCTTATCGAGAGCTTCAGGGTGGCAGCTAC 1458
 QY 1426 AAGGTGGAGATACACCGCTGTGGCGGACACACTGGAGATCATCAATGACACATCAGG 1485
 Db 1459 AAGAAGATTGGCTACTATGACAGCACCAGGATGATCTTCTGTTCCAAAACAGATAAA 1518
 QY 1486 TTCCAGGATCCGACCAACCAAGACAGACCATCATCTTGGAGCAGCTGCGGAAGATC 1545
 Db 1519 TGGATTGGAGGTTCCCGCCCGCTGACCAAGACCTTGGTATCATCAAGACATTCGGCTTCGT 1578
 QY 1546 TCCCTACCTCTCTACAGCATCTCTCTGCGCTTCAACCTCTCGGGATGATCAGGCCAGT 1605
 Db 1579 TCACAGAAACTCTTTATCTCCGCTCTCAGTTCTCTCCAGCTGGGCAATGTCTCCTAGCTTT 1638

QY 1606 GCTTTTCTCTTTTCAACATCAAGAACCGGAATCAGAGCTCAATAAAGATGTCAGTGCCA 1665
 Db 1639 GTCTGTCTGCTTTTAACTATCAAACTCAACATGTCCTGTTATATCCAGAACTCACAGCC 1698
 QY 1666 TACATGAACAACCTTATCATCTTGGAGGATGCTTTCTTATGCTTCCATATTTCTCTTT 1725
 Db 1699 AACCTGAACAACCTGACTGCTGTGGCTGCTCACTGGCTTTAGTGTGCTTCTCCCTGT 1758
 QY 1726 GGCCTTGATGATCCCTTTGTCTCTGAAAAGACCTTTTGAACACTTTGACCGTCAGGACC 1785
 Db 1759 GGGCTCGATGGTTACCAATTTGGAGGAACCAAGTTTCTCTTCGTCGCCAGCCGCCCTC 1818
 QY 1786 TGGATTCACCGTGGGCTACACGACCGCTTTTGGGGCCATGTTTGGCAAGACCTGGAGA 1845
 Db 1819 TGGCTCTCGGCTGGCTTTAGTCTGGCTACGCTTCCATGTTTCCACAGATTTGGTGG 1878
 QY 1846 GTCCAGGCCATCTTCAAAATCTGAANAATGAAGRA-----GAAGATCATCAAGGAC 1896
 Db 1879 GTCCACACGGTCTTCAAAAGAAAGAAAGAGAGAGTGGAGGAAGACTCTTGAACCC 1938
 QY 1897 CAGAAACTGCTTGTGATGCTGGGGGCTGCTGCTGATGACCTGTGTATCTCTGATCTGC 1956
 Db 1939 TGAAGCTGATGCCACAGTGGCCCTGCTGCTGGGCAATGATGCTCTCACTCTGCCCATC 1998
 QY 1957 TGGCAGGCTGTGGACCCCTCGGAAGGACAGTGGAGAAAGTACAGATGGAGCGGACCCA 2016
 Db 1999 TGGCAGATGCTGGACCTCTGCACCGGACCATTTGAGACATTTGCCAAGGAGGAACCTAAG 2058
 QY 2017 GCAGGACGGATATCCATCCGCTCTCTGGAGCACTGTGAGAACACCATATGACC 2076
 Db 2059 GAAGATATTGAGCTCTATTTCTGCCAGCTGGAGCAATTTGCAGCTCCAGGAAGTGAAT 2118
 QY 2077 ATCTGGCTTGGCATGCTCTATGCTTACAGGACCTTCTCATGTTTTCGGTGTGTTCTTA 2136
 Db 2119 ACATGCTTGGCATTTCTATGTTTACAGGGCTGCTGCTGCTGGGAATCTTCTT 2178
 QY 2137 GCTTGGGACACCGCAAGCTGACATCCCGCACTCAAGCAGACCAAGTACATCGGGATG 2196
 Db 2179 GCTTATGAGCAAGAGTGTGTCCACTGAGAAGATCAATGATCACCGGCTGTGGGCA 2238
 QY 2197 AGTGTCTCAAGCTGGGATCATGTGCATCATCGGGGCGCTGCTCTCTCTGACCCGG 2256
 Db 2239 GCTAATCAATGTGGCAGTCTGCTGCTCATCTGCTCTGTCACCATGATTTCTGTCC 2298
 QY 2257 GACCAAGCCCAATGTGAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2316
 Db 2299 AGCCAGCAGGATGCAGCCCTTGGCTTGTGCTCTCTTGGCATAGTTTCTCTCTCTATATC 2358
 QY 2317 ACCCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2360
 Db 2359 ACTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2402

RESULT 2
 V10265
 ID V10265 standard; cDNA to mRNA; 2620 BP.
 AC V10265;
 DT 03-JUN-1998 (first entry)
 DE Human GABA-BR1a/b receptor cDNA.
 KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
 KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
 KW epilepsy; cognitive function; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 CDS 1..2382
 FT /*tag= a
 FT /product= GABA-bR1a/b
 FN W09746675-A1.
 PD 11-DEC-1997.
 PF 19-MAR-1997; E01370.
 PR 22-NOV-1996; US-756091.
 PR 30-MAY-1996; US-655716.

QY 1052 GCTACATTGGCGTGGATTTCAGGCCCTGAGCTCCAAAGCAGATCAAGACCACTCTCAGGAA 1111
 Db 1440 GCCACATCACCACGGAGATTGTCATGCTGACCTGCCAACACCCGAGCATTTCCAAACA 1499
 QY 1112 AGACTCCACAGCATGATGAGAGAGATACAAACAAGCGGTACG-----CGTGGGGC 1165
 Db 1500 TGAGCTCAAGGAATTTGTGAGAGAACTAACCAAGCGCTGAAAGACACCCCGAGGAGA 1559
 QY 1166 CCAGCAAGTCCACGGTACCGCTACGATGCGATCTGGGTCAATCGCCCAAGACACTGCAGA 1225
 Db 1560 CTGGAGGCTTCCAGGAGCCACTGGCCTATGATGCTATCTGGGCCCTTGGCTTTGGCCT 1619
 QY 1226 GGGCCATGGAGACACTGATGCCAGCAGCGCCACAGCGGATCCAGGACTTCAACTACA 1285
 Db 1620 TGAACAAGACGCTGGAGGAGTGTGCTCCGCGGTGCGCTGGAGGACTTTAACTACA 1679
 QY 1286 CGGACCAACGCTGGCGAGGATCATCTCAATGCCATGAAGAGACCAACTTCTTGGGG 1345
 Db 1680 ACAACGACGACATTACAGACGAGATACCGGGCCATGAACCTCCTCCTCTTTGAGGGCG 1739
 QY 1346 TCACGGGTCAAGTTGATTTCCGGAATGGGAGAGAAATGGGACCATTAATTTACTCAAT 1405
 Db 1740 TTTCTGGCCATGTGCTTTGATGCCAGCGCTCCCGATGGCATGGACACTTATCGAGC 1799
 QY 1406 TTCAGACAGCAGGAGGTGAAGGTGGGAGATACAAAGCTGTGGCGGCACACACTGGAGA 1465
 Db 1800 AGCTACAGGCGCGAGCTACAAAGAGATCGGCTACTAGCAGACCAAGGATGATCTTT 1859
 QY 1466 TCATCAATGACACCATCATAGTTCCAAAGATCCGAACCAACCAAGACACCAATCATCC 1525
 Db 1860 CTTGTCCAAAACGACAAAGTGGATGGAGGGTCTCCCGCAGCTGACGACACTTTGTCTCA 1919
 QY 1526 TGGACGAGCTCGGAAGATCTCCCTACCTCTACAGCATCTCTCTGCGCTCACCATCC 1585
 Db 1920 TCAAGACATTCGTTCTGCTCAGAAACHTTTATCTCGGCTCAGTCTCTCCAGCC 1979
 QY 1586 TCGGATGATCATGCCAGTCTTTCTCTTCTTCAACATCAAGAACCGGAATCAGAAGC 1645
 Db 1980 TGGCATTTGCTTGTCTGCTGCTGCTTTTAACTACTCAACTCCACGCTTGGT 2039
 QY 1646 TCATAAAGATTCGAGTCCATACATGAACACCTTATCACTTTGGAGGATGCTTCCCT 1705
 Db 2040 ATATCCAGATCCCGACCCCAACCTGACAACTCTGCTGTGGGTGCTCTGCTGCGAC 2099
 QY 1706 ATGCTTCCATATTTCTTTTGGCTTGTATGATCCTTTGCTCTGAAAAGACCTTTGAAA 1765
 Db 2100 TGGCTGCTCTTCCCTCTCGGCTGGATGGTTTACCACATAGGAGAGCCAGTTCCTCGT 2159
 QY 1766 CACTTTGACCTTCAGGACCTTGGATTTCTACCGTGGGTACACGACCGCTTTTGGGGCCA 1825
 Db 2160 TTGCTCGCCAGCGCGCTTTTGGCTTTGGGCTTTAGTCTGGGCTATGGCTCTA 2219
 QY 1826 TGTTCGAAAGACCTGGAGATCCAGCCATCTTCAAAATGTGAAATGAAGAA----- 1881
 Db 2220 TGTTCGAAAGATCTGTGGGTCCACAGCTTTTCAAGAGAGGAGGAGGAGGAGT 2279
 QY 1881 ----GAAGATCATCAAGGACAGAACTGCTGTGATCGTGGGGGCGATGCTGTGATCG 1936
 Db 2280 GGAGGAAGACCTTAGAGCCCTGGAAACTATATGCCACTGTGGGCTCTGTTGGGCAATG 2339
 QY 1937 ACCTGTGATCCTGATCTGCTGGAGGCTGTGGACCCCTCTGCGAAGACAGTGGAGAGT 1996
 Db 2340 ATGCTCCTGACTTTGCCATCTGGCAGATTTGGACCCCTTTCACCCGAACCATTTGAGACT 2399
 QY 1997 ACAGCATGGAGCCGACCCAGCAGGAGGATATCTCCATCCGCCCTCTCTCTGGAGCACT 2056
 Db 2400 TTGCAAGGAGGAAACCAAGAGGAGACATCGATGTCTCCATCTCTCCCGCAGTGGAGACT 2459
 QY 2057 GTGAGAACACCATATGACCATCTGGCTTGGCATCGTCTATGCCCTACAGGGGACTTCTCA 2116
 Db 2460 GCAGCTCCAAAGATGATACGTGGCTTGGCATTTCTATGTTTACAGGGGCTGTGTC 2519

QY 2117 TGTGTTCCGGTTGTTTCTAGCTTTGGGAGACCCGCAACAGTCAGCATCCCGCACTCAACG 2176
 Db 2520 TGTCTCTGGGAATCTTTCTTCTTACGAAACCAAGAGCGTCTCCACTGAAAGATCAATG 2579
 QY 2177 ACAGCAAGTACATCGGATGAGTGTCTACACGCTGGGATCATGTGCATCATCGGGGCG 2236
 Db 2580 ACCACAGGCGCTGGGCATGGCTATCTACAATGTGCGGCTCTGTCTCATCACTGCTC 2639
 QY 2237 CTGTCTCTCTCTGACCCGCGGACGACCAATGTGCACTTCTGATCGTGGCTCTGGTCA 2296
 Db 2640 CHTGACCATGATCTTTCCAGTCAGGAGCAGCGCTTTGGCTTTGCCCTCTCTGGCCA 2699
 QY 2297 TCATCTTCTGACGACCATCACTCCCTCTGCTGTTGTTGTCGCGAAGCTCATCACTGTA 2356
 Db 2700 TCGTGTCTCTCTTCTTACATCACTCTGTTGTTGCTCTTTGTCGCCAAGATGGCAGGCTGA 2759
 QY 2357 GAAC 2360
 Db 2760 TCAC 2763

RESULT 5
 V88919
 ID V88919 standard; cDNA; 314 BP.
 AC V88919;
 DT 12-FEB-1999 (first entry)
 DE EST clone HW456.
 KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
 KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
 KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
 KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 OS Homo sapiens.
 PN W09845437-A2.
 PD 15-OCT-1998.
 PE 10-APR-1998; U06956.
 PR 10-APR-1997; US-837312.
 PA (GENY) GENETICS INST INC.
 PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
 PI Racie LA, Spaulding V, Treacy M;
 DR WPI: 99-070078/06.
 PT New polynucleotides encoding human secreted proteins - derived from
 PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
 PT ovary, pituitary, retina and colon cDNA libraries
 PS Claim 1; Page 556-557; 641pp; English.
 CC The present sequence represents an expressed sequence tag (EST), and is
 CC a polynucleotide of the invention. The polynucleotides of the invention
 CC are all secreted EST sequences isolated from a variety of human tissue
 CC sources. The EST sequences and proteins encoded by them are predicted to
 CC have useful biological activities which would make them suitable for
 CC treating, preventing or ameliorating medical conditions in humans and
 CC animals, although no supporting data is given. Suggested activities
 CC include nutritional activity, immune stimulating or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity. The EST sequences are also stated to be useful for gene
 CC therapy.
 SQ Sequence 314 BP; 72 A; 81 C; 89 G; 72 T;

Query Match 8.8%; Score 286.8; DB 1; Length 314;
 Best Local Similarity 97.7%; Pred. No. 3.6e-61;
 Matches 291; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1857 CTTCAAAATGTGAAATCAAGACAGATCATCAAGCACCAGAACTGCTGTGATCGT 1916
 Db 10 CTTCTAGGCTAGAAATGAAGAGAAATCATCAAGGACCAGAACTGCTGTGATCGT 69
 QY 1917 GGGGGGCATGCTGCTGATCGACCTGTGATCTGCTGCTGGCAGGCTGTGGACCCCT 1976
 Db 70 GGGGGGCATGCTGCTGATCGACCTGTGATCTGCTGCTGGCAGGCTGTGGACCCCT 129

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QY 1977 GCGAAGACAGTGGAGAGTACAGCATGGAGCCGGACCCAGACAGCGGATATCTCCAT 2036
      |||||||
Db 130 GCGAAGGACAGTGGAGAAATACAGATGGAGCCGGACCCAGACAGCGGATATCTCCAT 189
      |||||||
QY 2037 CGGCCCTCTCTGGAGCACTGTGAGAACACCCATATGACCATCTGGCTTGGCATCGTCTA 2096
      |||||||
Db 190 CGGCCCTCTCTGGAGCACTGTGAGAACACCCATATGACCATCTGGCTTGGCATCGTCTA 249
      |||||||
QY 2097 TGCTTACAGGACATCTCATGTGTGTTGGTGTGTTCTTAGCTTGGGAGACCCGCAAC 2154
      |||||||
Db 250 TGCTTACAGGACATCTCATGTGTGTTGGTGTGTTCTTAGCTTGGGAGACCCGCAAC 307
      |||||||
RESULT 6
X51891
ID X51891 standard; DNA: 361 BP.
AC X51891.
DT 22-JUN-1999 (first entry)
DE Human secreted protein 5', EST SEQ ID NO: 105.
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
OS Homo sapiens.
PN WO9906552-A2.
PD 11-FEB-1999.
PF 31-JUL-1998; IB1236.
PR 01-AUG-1997; US-905223.
PA (GEST ) GENSET.
PI Duclert A, Dumas Maline Edwards J, Lacroix B;
DR WPI; 99-153782/13.
DR P-PSDB; Y13091.
PT New isolated brain-derived nucleic acids - used to develop products
PT which may have cytokine, immune, regulatory, haematopoiesis
PT regulating, anti-inflammatory or tumour inhibition activity
PS Claim 1; Page 253; 57pp; English.
CC X51787 to X52019 represent 5' expressed sequence tags (ESTs) for human
CC secreted proteins, and encode the proteins given in Y12987 to Y13219,
CC respectively. The proteins given represent the signal peptide and an
CC N-terminal fragment of a secreted protein. The nucleic acid sequences
CC can be used for producing secreted human gene products. They can also
CC be used to develop products for diagnosis and therapy. The proteins
CC obtained may have cytokine activity, cell proliferation/differentiation
CC activity, haematopoiesis regulating activity, tissue growth regulating
CC activity, reproductive hormone regulating activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, tumour inhibition activity
CC or other activities. The products can be used in forensic, gene therapy
CC and chromosome mapping procedures. The sequences can also be used for
CC obtaining corresponding promoter sequences. The nucleic acids encoding
CC the signal peptide can be used for directing extracellular secretion of
CC a polypeptide or the insertion of a polypeptide into a membrane, or
CC importing a polypeptide into a cell.
SQ Sequence 361 BP; 86 A; 94 G; 92 T;

Query Match 5.5%; Score 177; DB 1; Length 361;
Best Local Similarity 90.4%; Pred. No. 2.9e-34;
Matches 189; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 404 ACTTCCTCGACCTGGGCTCTATGACAGCGGAGTGGCAACGCAAAAGGGTTGAAGCCT 463
      |||||
Db 153 AGTCATCTATTGGAGCGGCAATCATGTCAGTGGGACACGCAAAAGGGTTGAAGCCT 212
      |||||
QY 464 TCTAGATGCGATAAATACGGGGCGAACCACTTGATGTTGTTTGGAGGCGTCTGTCCAT 523
      |||||||
Db 213 TCTAGATGCAATAAATACGGGGCGTAACCACTTGATGTTGTTTGGAGGCGTCTGTCCAT 272
      |||||||
QY 524 CCGTCACATCATCATTCGACAGTCCCTCCAGGCTGGAATCTGGTGCAGGTTTCTTTG 583
      |||||||
Db 273 CGGTCACATCATCATTCGACAGTCCCTCCAGGCTGGAATCTGGTGCAGGTTTCTTTG 332
      |||||||
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QY 584 CTGCAACCACGCGCTGTCTAGCCGATAAG 612
      |||||||
Db 333 CTGCAACCACGCGCTGTCTAGCCGATAAG 361
      |||||||
RESULT 7
Q11726
ID Q11726 standard; DNA: 2176 BP.
AC Q11726.
DT 25-JUN-1991 (first entry)
DE Sequence encoding viral reverse transcriptase enzyme.
KW Reverse transcriptase; HIV; HTLV-I; ss.
OS Myxococcus xanthus.
FH Key Location/Qualifiers
FT cds 640..2097
FT /*tag= a
FT /product= viral reverse transcriptase
PN J03022975-A.
PD 31-JAN-1991.
PF 22-FEB-1990; 042305.
PR 24-FEB-1989; US-315316.
PA (UYNE-) Univ of New Jersey.
DR WPI; 91-127415/18.
DR P-PSDB; R11919.
PT Novel protein having reverse transcriptase enzyme activity -
PT obtd. by culturing Myxococcus xanthus FB
PS Disclosure; fig 4; 9pp; Japanese.
CC This sequence encodes a protein with viral (e.g. HIV or HTLV-I)
CC reverse transcriptase enzyme activity and is extracted from
CC Myxococcus xanthus. See also J03022976.
SQ Sequence 2176 BP; 340 A; 763 C; 789 G; 284 T;

Query Match 1.4%; Score 45.4; DB 1; Length 2176;
Best Local Similarity 50.6%; Pred. No. 0.1;
Matches 135; Conservative 0; Mismatches 131; Indels 1; Gaps 1;

QY 149 GGAGTCGAGGGCGGAGGAGAGCGCGTGAGTGAGCAGATGCAGAGCGGTGCGGCCCA 208
      |||||
Db 891 GAAGGCTTGAGAGGAGAGAGAGCGCGAGCGGCGCGCCCTCTGAAGCGTCA 950
      |||||
QY 209 GAATCGCGCTCGGCCCGTGCACCCCGCGCCATGCCAGTTGCCCGCGCGCTCTG 268
      |||||
Db 951 GCGGCACAGGGGTGGAAGCGCCACGACGTGGCCACCTGCGCCGCCCTCG 1009
      |||||
QY 269 CTACGGGCGCGCTCTCTCATCATGGGCGCTATCGCGCTACCAAGGAGGTGGCAAGGCA 328
      |||||
Db 1010 CGGAGGACCCCTTGGCGGACGGGTTTCGAGTGGCCCGCGGAGGAGCGCGCGGCCA 1069
      |||||
QY 329 GCATCGGGCGGCTGTGCTCCCGCGGTGAACTGGCCATCGAGCAGATCCGCAACGAGT 388
      |||||
Db 1070 ACGGCTGAGGAGCTGGACTCGGGGAGGCGCTGGCCAAGGCGCTGGGGCTTGACCGTGT 1129
      |||||
QY 389 CACTCTCTGCGCCCTTACTTCTCTGACC 415
      |||||
Db 1130 CCAAGCTGCGTGGTTCGCGTTCACC 1156
      |||||

RESULT 8
X51965
ID X51965 standard; DNA: 397 BP.
AC X51965.
DT 22-JUN-1999 (first entry)
DE Human secreted protein 5', EST SEQ ID NO: 179.
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
OS Homo sapiens.
PN WO9906552-A2.
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